

## SEQUENCE LISTING

&lt;110&gt; Aarhus Universitet

&lt;120&gt; Method for determining predisposition to manifestation of immune system related diseases

&lt;130&gt; P 706 DK 02

&lt;160&gt; 8

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 671

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens; mature MASP-2

&lt;400&gt; 1

Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala  
1 5 10 15

Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp  
20 25 30

Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His  
35 40 45

Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu  
50 55 60

Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr  
65 70 75 80

Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser  
85 90 95

Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe  
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln  
115 120 125

Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His  
130 135 140

Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg  
145 150 155 160

Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln  
 165 170 175

Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys  
 180 185 190

Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val  
 195 200 205

Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr  
 210 215 220

Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His  
 225 230 235 240

Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser  
 245 250 255

Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr  
 260 265 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro  
 275 280 285

Met Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile  
 290 295 300

Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu  
 305 310 315 320

Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp  
 325 330 335

Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly  
 340 345 350

Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro  
 355 360 365

Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr  
 370 375 380

Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp  
 385 390 395 400

Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu  
405 410 415

Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly  
420 425 430

Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu  
435 440 445

Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu  
450 455 460

Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu  
465 470 475 480

Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln  
485 490 495

Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala  
500 505 510

Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val  
515 520 525

Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu  
530 535 540

Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu  
545 550 555 560

Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro  
565 570 575

Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr  
580 585 590

Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser  
595 600 605

Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe  
610 615 620

Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp

625                                  630                                  635                                  640

Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val Tyr Thr Lys  
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Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser Asp Phe  
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<210> 2  
<211> 170  
<212> PRT  
<213> mature MAp-19 (human)

<400> 2

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Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp  
                                20                                  25                                  30

Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His  
                                35                                  40                                  45

Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu  
                                50                                  55                                  60

Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr  
65                                  70                                  75                                  80

Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser  
                                85                                  90                                  95

Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe  
                                100                                  105                                  110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln  
                                115                                  120                                  125

Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His  
                                130                                  135                                  140

Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg  
145                                  150                                  155                                  160

Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu

165

170

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<211> 2061  
<212> DNA  
<213> cDNA MASP-2

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aatgaccagg agcggcgctg gaccctgact gcaccccccg gctaccgcct gcgcctctac 180  
ttcaccact tcgacctgga gctctccac ctctgcgagt acgacttcgt caagctgagc 240  
tcgggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcggggc 300  
cctggcaagg acactttcta ctgcgtgggc tccagcctgg acattacctt ccgctccgac 360  
tactccaacg agaagccgtt cacgggggtc gaggccttct atgcagccga ggacattgac 420  
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tgtccctacg acttttctca gattcaaaca gacagagaag aacatggccc attctgtggg 780  
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acaggagggc gtatatatgg agggcaaaag gcaaacctg gtgattttcc ttggcaagtc 1380  
ctgatattag gtggaaccac agcagcaggt gcacttttat atgacaactg ggtcctaaca 1440  
gctgctcatg ccgtctatga gcaaaaacat gatgcatccg ccctggacat tcgaatgggc 1500

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accctgaaaa gactatcacc tcattataca caagcctggt ctgaagctgt ttttatacat 1560
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aaagttgtaa tcaatagcaa catcacgcct atttgtctgc caagaaaaga agctgaatcc 1680
tttatgagga cagatgacat tggaactgca tctggatggg gattaaccca aaggggtttt 1740
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gcatatgaaa agccacccta tccaagggga agtghtaactg ctaacatgct ttgtgctggc 1860
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<210> 4  
 <211> 558  
 <212> DNA  
 <213> cDNA MAp-19

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aatgaccagg agcggcgctg gaccctgact gcaccccccg gctaccgcct gcgcctctac 180
ttcaccact togacctgga gctctccac ctctgcgagt acgacttcgt caagctgagc 240
tcgggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcgggcc 300
cctggcaagg acactttcta ctgctgggc tccagcctgg acattacctt ccgctccgac 360
tactccaacg agaagccgtt cacgggggttc gaggccttct atgcagccga ggacattgac 420
gagtgccagg tggccccggg agaggcgccc acctgcgacc accactgcca caaccacctg 480
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tcagagcaga gcctctag 558

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<210> 5  
 <211> 21  
 <212> DNA  
 <213> upper PCR primer

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<400> 5
gcgagtacga cttcgtcaag g 21

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<210> 6  
 <211> 21

<212> DNA  
<213> lower PCR primer

<400> 6  
ctcggctgca tagaaggcct c

21

<210> 7  
<211> 21  
<212> DNA  
<213> upper PCR primer

<400> 7  
ccagaccttt ggaaagttag c

21

<210> 8  
<211> 21  
<212> DNA  
<213> lower PCR primer

<400> 8  
ggctcaagtt ccaagtattg c

21